ifestations of disease were fever (84.2%), arthralgia (81.2%), perspiration (60.2%), lack of appetite (54%), Hepatomegaly (31%), splenomegaly (21%), and lympadenopathy (18%). Laboratory findings were anemia (52.3%), leucopenia (41.2%), thrombocytopenia (4.5%), and leukocytosis (1.96%). Treatment in the majority of patients (76.2%) was Cotrimoxazole besides Rifampin or Gentamycin. The brucellosis was the cause of FUO in the 17.6% of cases.
Conclusion: According to the findings, it seems that among children with fever and Arthralgia and especially with precedence of non-pasteurized dairy consumption and being male, this is essential to evaluate brucellosis possibilities. On the other hand, it is advised to perform programs to inform members of high risk families about this disease.

PP-009 Molecular epidemiology of community-acquired, methicillin-resistant *Staphylococcus aureus* infections in children in China

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Background: Community-associated meticillin-resistant Staphylococcus aureus (CA-MRSA) has emerged worldwide since 1990s.
Methods: Ninety-nine MRSA isolates were analyzed by multilocus sequence typing (MLST), SCCmec typing and spa typing. Panton-Valentine Leukocin (PVL) gene was detected. Susceptibility tests were performed for twelve antimicrobial agents.
Result: Eleven sequence types (STs) were identified. The predominant SCCmec types were type IV (77.1%) and type V (22.9%). SCCmec type IVA, IVc, IVg were found. All strains were differentiated into twelve spa types, 57.6% (57/99) of MRSA isolates were found to carry the PVL gene. The prevalent strains were ST59-MRSA-IVA and ST59-MRSA-V. Four ST910 and ST338 isolates were found countrywide, ST1349 were found from healthy children. Multidrug resistance was observed.
Conclusion: ST59, ST910-MRSA-IV and ST910-MRSA-V were spread all of China, and ST338 was also found in south of China. Isolates from healthy Children had different genetic background.

PP-010 Determination of prevalence antibiotic resistance of isolated bacteria from tracheal aspirated in intubated patients admitted to intensive care unit at Toohid hospital, Sanandaj in Iran

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Background: Low respiractory tract infection is the first agent mortality in nosocomial infection, and among ICU patients are 5-10 time higher than other ward.
The aim of this study was determination of prevalence and antibiotic resistance of bacteria isolates from tracheal aspirated in intubated patients admitted in ICU ward
Material & methods: This is prospective descriptive study included 185 specimens of secretion respiratory tract admited to ICU during a period of 13 month 2006/4/1 to 2007/5/1.
In order to isolation bacterial the specimens were cultured in enrichment and differential media. The data analyzed by means of SPPSS- win software.
Results: 112 (60.3%) of 185 specimens had culture positive. Prevalent microbial agent in this group were: Enterobacter 19.6%, Pseudomonas spp, 19.6%, Serratia 18.8%, klebsiella 15.2%, E. coli 10.7% and staphylococcus 4.5%. Iisolated bacteria resistance to often antibiotics and highest resistant to amoxiciline. Prevalence of Acinetobacter with age over 40 year and sex (female) ($p<0.05$) and also prevalence of entrobacter and serratia with history of previous antibiotic use ($p=0.2$, $p<0.05$) has showed a signification statistically correlations.
Conclusion: This studuy shows that gram negative bacteria have high prevalence in patients admitted to ICU. The increased of these species in most cases due to administration of inadequate and irrational antimicrobial thrapy.To overcome this problem it needs to develop new antimicrobial and increasing compliance.

PP-011 High level macrolide resistant *Streptococcus pyogenes* Isolated from Chinese children and the relationship with Tn*6002*

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Background: The macrolide resistance rate in Chinese had been reported. This research was to investigate the high level macrolide resistant *Streptococcus pyogenes* in Chinese children. A total of 191 streptococcus pyogenes were contained.
Methods: Susceptibility to 11 antibiotics were detected, together with the Macrolide resistance phenotype of the strains. Macrolide resistance genes (*ermB*, *ermTR*, *mefA*), tetracycline resistance gene (*tetM*, *tetO*), *int*, *xis* of Tn*916* family and also two special fragments of Tn*6002* were detected by PCR and sequencing.
Result: Among the 191 isolates, 87.93% were resistant to telithromycin, 92.63% were resistant to tetracycline, none of the isolates were resistant to penicillin G, ceftazidime, levofloxacin and trimethoprim-sulfamethoxazole. And all of the isolates belong to the cMLS phenotype. 95.81% (183/191) of the 191 strains had the *ermB* gene, 4.19% (8/191) of the isolates contained the *ermTR* gene, *mefA* was not detected. Among the *ermB* positive strains, 92.35% (169/183) of them carried the *tetM* gene, 93.99% (172/183) was positive for the genes of *int* or *xis*. *ErmB*, *tetM*, *int*, *xis* positive profile account for 86.91% (166/191) of the 191 strains and all of them carried the special fragment of Tn*600*.
Conclusion: This study indicated that there may be a high preverlance of transposion Tn*6002* carrying *ermB* gene among high level macrolide resistant *Streptococcus pyogenes* from Chinese children.

PP-012 Novel blaCTX-M-79 gene from community isolates in association with ISEcp1 in Shenyang, China

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Objectives: This study was conducted to analysis the IS*Ecp1* element in association with *bla*CTX-M genes in a community ESBL producing E coli isolates.
Methods: 19 *Escherichia coli* producing CTX-M-type β-lactamase were collected from five communities in elderly people in Shenyang, China. PCR amplification and direct sequencing was used to detect the insertion sequence IS*Ecp1* element in genetic environment *bla*CTX-M genes.
Results: IS*Ecp1*element was associated with several *bla*CTX-M types, such as CTX-M-14, CTX-M-24, CTX-M-22, and CTX-M-79. Sequence analysis revealed that all these IS*Ecp1*-like DNA sequences contained the putative promoter region involved in the transcription of *bla* CTX-M genes. IS*Ecp1* insertion sequences have been observed 42-127 bp upstream of the ORFs encoding the CTX-M enzymes in all 19 strains. CTX-M-79 β-lactamase encoding gene was observed with different insertion site of IS*Ecp1* and variable sequences between the IS*Ecp1* and *bla*CTX-M-79 gene. For one strain (T298) IS*Ecp1*element was disrupted by IS10.
Conclusions: This work confirmed the IS*Ecp1* elements were closely related to *bla*CTX-M genes in community isolates in Shenyang, China.